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General Information

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Systematic Name SPAC1F8.07c

Status role inferred from homology

Product pyruvate decarboxylase (predicted)

Type CDS

Sequence DNA and Protein

Location

Chromosome 1

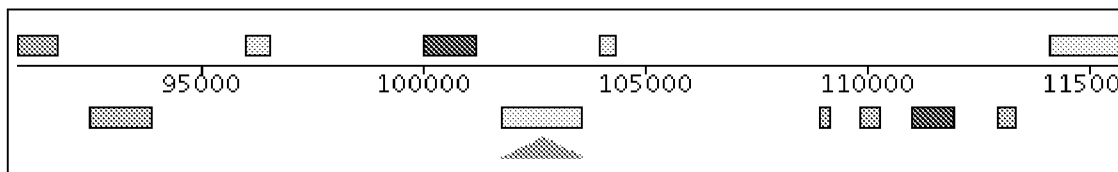
Contig Location complement(101760..103544) (Unspliced length: 1785 bp)

Exons complement(101760..103544) (Spliced length: 1785 bp)

[Region download and display \(in Artemis\)](#)

[Genome Browser](#)

Context Map:



SPNCRNA.139 SPAC1F8.04c [isp3](#) [fta5](#) >SPAC1F8.07c< SPAC1F8.08 SPAC11D3.01c SPAC11D3.02c
SPAC11D3.03c SPAC11D3.04c [mfs2](#)

Curation

Term conserved protein
similar to *S. pombe* [SPAC186.09](#) (paralog)

Other genes annotated to this term
(81 Others)
(0 Others)

Predicted Peptide Properties

Mass	64.7 kDa	Amino acids	594
Isoelectric point	pH 5.9	Charge	-4.5
Signal Peptide	Not found		
Transmembrane Domains	0 found		
GPI Anchor	Not found		

Gene Ontology Annotation

Term (browse Amigo)	Qualifier Evidence	Other genes annotated to this term
Biological Process		
generation of precursor metabolites and energy	NAS	120 others
pyruvate metabolic process	ISS (PMID:17072883) with Interpro:IPR012110	25 others
Molecular Function		
magnesium ion binding	IEA (GOA:interproGO_REF:0000002) with InterPro:IPR000399	89 others
pyruvate decarboxylase activity	ISS (PMID:17072883) with Interpro:IPR012110	3 others
thiamin pyrophosphate binding	IEA (GOA:interproGO_REF:0000002) with InterPro:IPR000399	6 others
transferase activity	IEA (GOA:interproGO_REF:0000002) with InterPro:IPR000399	645 others

Catalytic Activity

EC 4.1.1.1 : [IUBMB](#)

Published Expression Profiles

Gene Expression Viewer [Cell Cycle](#) [Meiosis](#) [Environmental Stress](#) [Pheromone Response/Mating](#)
 TranscriptomeViewer [SPAC1F8.07c](#) [High-resolution view of transcripts in neighbourhood](#)

Literature

Search for in [PubMed](#)

Domain Information

[View Pfam domain structure for this gene product](#)

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DB	Accs	Description
Pfam	PF02776	Thiamine pyrophosphate enzyme, N-terminal TPP binding domain
Pfam	PF00205	Thiamine pyrophosphate enzyme, central domain
Pfam	PF02775	Thiamine pyrophosphate enzyme, C-terminal TPP binding domain
InterPro	IPR012110	Pyruvate decarboxylase/indolepyruvate decarboxylase
InterPro	IPR000399	TPP-binding enzymes
InterPro	IPR012001	Thiamine pyrophosphate enzyme, N-terminal TPP binding region
InterPro	IPR011766	Thiamine pyrophosphate enzyme, C-terminal TPP-binding
InterPro	IPR012000	Thiamine pyrophosphate enzyme, central region
PROSITE	PS00187	Thiamine pyrophosphate enzymes signature.

Database Cross-References

DB	Accs	Description
UniProtKB	Q92345	Probable pyruvate decarboxylase C1F8.07c (EC 4.1.1.1).
EMBL	CU329670	Schizosaccharomyces pombe chromosome I
Biotwiki	SPAC1F8_07c	Biotwiki
NCBI Entrez Gene	SPAC1F8.07c	NCBI Entrez Gene
FYSSION	SPAC1F8.07c	FYSSION
GermOnline	SPAC1F8.07c	GermOnline

NBRP [SPAC1F8.07c](#) Fission yeast strain database, National BioResource Project (Japan)
 PIR [T38114](#) PIR
 YOGY [SPAC1F8.07c](#) Retrieval of eukaryotic orthologs

UniProtKB Annotation For This Protein

Catalytic Activity A 2-oxo acid = an aldehyde + CO(2).
 Cofactor Binds 1 metal ion per subunit. ; Binds 1 thiamine pyrophosphate per subunit.
 Similarity Belongs to the TPP enzyme family.
 Subunit Homotetramer (By similarity).
 Keywords Complete proteome ([4982 others](#)), Decarboxylase ([11 others](#)), Flavoprotein ([45 others](#)),
 Lyase ([60 others](#)), Magnesium ([81 others](#)), Metal-binding ([451 others](#)), Thiamine
 pyrophosphate ([11 others](#))

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